

SEQUENCE LISTING



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SHIMBA, NOBUHISA
MIHARA, YASUHIRO
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KURAHASHI, OSAMU
KOUHA, TOHRU
SHIMAOKA, MEGUMI
KOZUTSUMI, RIE
ASANO, YASUHISA

<120> MUTANT NUCLEOSIDE-5'-PHOSPHATE PRODUCING ENZYMES

<130> 206523USOPCT

<140> 09/807,990

<141> 2000-09-01

<150> JP 11/249545

<151> 1999-09-03

<160> 125

<170> PatentIn version 3.3

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<213> Escherichia blattae

<220>

<221> CDS

<222> (331)..(1077)

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cgcggggggt ccccgggccg ctttttttta tggggctgcg gtgaggagcg ttatctgctg	180
gccctgtttg tgcaacaac gcttttattg tgtaatttt gtgacgtata tcaggttttt	240
aagcaccctg tggcgctcat actggcaacc tgttgatatt aagcaacact cttcactcac	300
ggaattaaca cgacacagtaa aggtatacgc atg aaa aaa cgt gtt ctg gca gtt	354
Met Lys Lys Arg Val Leu Ala Val	

tgt ttt gcc gca ttg ttc tct tct cag gcc ctg gcg ctg gtc gct acc 402
 Cys Phe Ala Ala Leu Phe Ser Ser Gln Ala Leu Ala Leu Val Ala Thr
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ggc aac gac act acc acg aaa ccg gat ctc tac tac ctc aag aac agt 450
 Gly Asn Asp Thr Thr Lys Pro Asp Leu Tyr Tyr Leu Lys Asn Ser
 25 30 35 40

gaa gcc att aac agc ctg gcg ctg ttg ccg cca cca ccg gcg gtg ggc 498
 Glu Ala Ile Asn Ser Leu Ala Leu Leu Pro Pro Pro Ala Val Gly
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tcc att gcg ttt ctc aac gat cag gcc atg tat gaa cag ggg cgc ctg 546
 Ser Ile Ala Phe Leu Asn Asp Gln Ala Met Tyr Glu Gln Gly Arg Leu
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ctg cgc aac acc gaa cgc ggt aag ctg gcg gcg gaa gat gca aac ctg 594
 Leu Arg Asn Thr Glu Arg Gly Lys Leu Ala Ala Glu Asp Ala Asn Leu
 75 80 85

agc agt ggc ggg gtg gcg aat gct ttc tcc ggc gcg ttt ggt agc ccg 642
 Ser Ser Gly Gly Val Ala Asn Ala Phe Ser Gly Ala Phe Gly Ser Pro
 90 95 100

atc acc gaa aaa gac gcc ccg gcg ctg cat aaa tta ctg acc aat atg 690
 Ile Thr Glu Lys Asp Ala Pro Ala Leu His Lys Leu Leu Thr Asn Met
 105 110 115 120

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 Ile Glu Asp Ala Gly Asp Leu Ala Thr Arg Ser Ala Lys Asp His Tyr
 125 130 135

atg cgc att cgt ccg ttc gcg ttt tat ggg gtc tct acc tgt aat acc 786
 Met Arg Ile Arg Pro Phe Ala Phe Tyr Gly Val Ser Thr Cys Asn Thr
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acc gag cag gac aaa ctg tcc aaa aat ggc tct tat ccg tcc ggg cat 834
 Thr Glu Gln Asp Lys Leu Ser Lys Asn Gly Ser Tyr Pro Ser Gly His
 155 160 165

acc tct atc ggc tgg gct act gcg ctg gtg ctg gca gag atc aac cct 882
 Thr Ser Ile Gly Trp Ala Thr Ala Leu Val Leu Ala Glu Ile Asn Pro
 170 175 180

cag cgc cag aac gag atc ctg aaa cgc ggt tat gag ctg ggc cag agc 930
 Gln Arg Gln Asn Glu Ile Leu Lys Arg Gly Tyr Glu Leu Gly Gln Ser
 185 190 195 200

cgg gtg att tgc ggc tac cac tgg cag agt gat gtg gat gcc gcg cgg 978

Arg Val Ile Cys Gly Tyr His Trp Gln Ser Asp Val Asp Ala Ala Arg
 205 210 215

gta gtg gga tct gcc gtt gtg gcg acc ctg cat acc aac ccg gcg ttc 1026
 Val Val Gly Ser Ala Val Val Ala Thr Leu His Thr Asn Pro Ala Phe
 220 225 230

cag cag cag ttg cag aaa gcg aag gcc gaa ttc gcc cag cat cag aag 1074
 Gln Gln Gln Leu Gln Lys Ala Lys Ala Glu Phe Ala Gln His Gln Lys
 235 240 245

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 35 40 45

Leu Pro Pro Pro Pro Ala Val Gly Ser Ile Ala Phe Leu Asn Asp Gln
 50 55 60

Ala Met Tyr Glu Gln Gly Arg Leu Leu Arg Asn Thr Glu Arg Gly Lys
 65 70 75 80

Leu Ala Ala Glu Asp Ala Asn Leu Ser Ser Gly Gly Val Ala Asn Ala
 85 90 95

Phe Ser Gly Ala Phe Gly Ser Pro Ile Thr Glu Lys Asp Ala Pro Ala
 100 105 110

Leu His Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala
 115 120 125

Thr Arg Ser Ala Lys Asp His Tyr Met Arg Ile Arg Pro Phe Ala Phe
 130 135 140

Tyr Gly Val Ser Thr Cys Asn Thr Thr Glu Gln Asp Lys Leu Ser Lys
 145 150 155 160

Asn Gly Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala
 165 170 175

Leu Val Leu Ala Glu Ile Asn Pro Gln Arg Gln Asn Glu Ile Leu Lys
 180 185 190

Arg Gly Tyr Glu Leu Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp
 195 200 205

Gln Ser Asp Val Asp Ala Ala Arg Val Val Gly Ser Ala Val Val Ala
 210 215 220

Thr Leu His Thr Asn Pro Ala Phe Gln Gln Gln Leu Gln Lys Ala Lys
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Ala Glu Phe Ala Gln His Gln Lys Lys
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 catcaaaaat acttacctgt cttccgtctg tttcgtcaca cttttttgaa agagttaaca 240
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 Leu Phe Ser Leu Ser Ala Leu Ala Ala Ile Pro Ala Gly Asn Asp Ala
 15 20 25
 acc acc aag ccg gat tta tat tat ctg aaa aat gaa cag gct atc gac 447
 Thr Thr Lys Pro Asp Leu Tyr Tyr Leu Lys Asn Glu Gln Ala Ile Asp
 30 35 40
 agc ctg aaa ctg tta ccg cca ccg ccg gaa gtc ggc agt att cag ttt 495
 Ser Leu Lys Leu Leu Pro Pro Pro Pro Glu Val Gly Ser Ile Gln Phe
 45 50 55 60
 tta aat gat cag gca atg tat gag aaa ggc cgt atg ctg cgc aat acc 543
 Leu Asn Asp Gln Ala Met Tyr Glu Lys Gly Arg Met Leu Arg Asn Thr
 65 70 75
 gag cgc gga aaa cag gca cag gca gat gct gac ctg gcc gca ggg ggt 591
 Glu Arg Gly Lys Gln Ala Gln Ala Asp Ala Asp Leu Ala Ala Gly Gly
 80 85 90
 gtg gca acc gca ttt tca ggg gca ttc ggc tat ccg ata acc gaa aaa 639
 Val Ala Thr Ala Phe Ser Gly Ala Phe Gly Tyr Pro Ile Thr Glu Lys
 95 100 105
 gac tct ccg gag ctg tat aaa ctg ctg acc aat atg att gag gat gcc 687
 Asp Ser Pro Glu Leu Tyr Lys Leu Leu Thr Asn Met Ile Glu Asp Ala
 110 115 120
 ggt gat ctt gcc acc cgc tcc gcc aaa gaa cat tac atg cgc atc ccg 735
 Gly Asp Leu Ala Thr Arg Ser Ala Lys Glu His Tyr Met Arg Ile Arg
 125 130 135 140
 ccg ttt gcg ttt tac ggc aca gaa acc tgt aat acc aaa gat cag aaa 783
 Pro Phe Ala Phe Tyr Gly Thr Glu Thr Cys Asn Thr Lys Asp Gln Lys
 145 150 155
 aaa ctc tcc acc aac gga tct tac ccg tca ggt cat acg tct atc ggc 831

Lys Leu Ser Thr Asn Gly Ser Tyr Pro Ser Gly His Thr Ser Ile Gly
 160 165 170
 tgg gca acc gca ctg gtg ctg gcg gaa gtg aac ccg gca aat cag gat 879
 Trp Ala Thr Ala Leu Val Leu Ala Glu Val Asn Pro Ala Asn Gln Asp
 175 180 185
 gcg att ctg gaa cgg ggt tat cag ctc gga cag agc cgg gtg att tgc 927
 Ala Ile Leu Glu Arg Gly Tyr Gln Leu Gly Gln Ser Arg Val Ile Cys
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 ggc tat cac tgg cag agt gat gtg gat gcc gcg cgg att gtc ggt tca 975
 Gly Tyr His Trp Gln Ser Asp Val Asp Ala Ala Arg Ile Val Gly Ser
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 Ala Ala Val Ala Thr Leu His Ser Asp Pro Ala Phe Gln Ala Gln Leu
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 240 245
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 35 40 45

Leu Pro Pro Pro Pro Glu Val Gly Ser Ile Gln Phe Leu Asn Asp Gln
50 55 60

Ala Met Tyr Glu Lys Gly Arg Met Leu Arg Asn Thr Glu Arg Gly Lys
65 70 75 80

Gln Ala Gln Ala Asp Ala Asp Leu Ala Ala Gly Gly Val Ala Thr Ala
85 90 95

Phe Ser Gly Ala Phe Gly Tyr Pro Ile Thr Glu Lys Asp Ser Pro Glu
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Leu Tyr Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala
115 120 125

Thr Arg Ser Ala Lys Glu His Tyr Met Arg Ile Arg Pro Phe Ala Phe
130 135 140

Tyr Gly Thr Glu Thr Cys Asn Thr Lys Asp Gln Lys Lys Leu Ser Thr
145 150 155 160

Asn Gly Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala
165 170 175

Leu Val Leu Ala Glu Val Asn Pro Ala Asn Gln Asp Ala Ile Leu Glu
180 185 190

Arg Gly Tyr Gln Leu Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp
195 200 205

Gln Ser Asp Val Asp Ala Ala Arg Ile Val Gly Ser Ala Ala Val Ala
210 215 220

Thr Leu His Ser Asp Pro Ala Phe Gln Ala Gln Leu Ala Lys Ala Lys
225 230 235 240

Gln Glu Phe Ala Gln Lys Ser Gln Lys

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 <222> (132)..(827)

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agtgagtctt t atg aaa agt cgt tat tta gta ttt ttt cta cca ctg atc 170
               Met Lys Ser Arg Tyr Leu Val Phe Phe Leu Pro Leu Ile
               1               5               10

gta gct aaa tat aca tca gca gaa aca gtg caa ccc ttt cat tct cct 218
Val Ala Lys Tyr Thr Ser Ala Glu Thr Val Gln Pro Phe His Ser Pro
15               20               25

gaa gaa tca gtg aac agt cag ttc tac tta cca cca ccg cca ggt aat 266
Glu Glu Ser Val Asn Ser Gln Phe Tyr Leu Pro Pro Pro Pro Gly Asn
30               35               40               45

gat gat ccg gct tac cgc tat gat aag gag gct tat ttt aag ggc tat 314
Asp Asp Pro Ala Tyr Arg Tyr Asp Lys Glu Ala Tyr Phe Lys Gly Tyr
50               55               60

gcg ata aag ggt tcc ccg cga tgg aaa caa gct gct gag gat gca gat 362
Ala Ile Lys Gly Ser Pro Arg Trp Lys Gln Ala Ala Glu Asp Ala Asp
65               70               75

gta agc gtg gaa aat ata gcc aga ata ttc tcg cca gta gtg ggt gct 410
Val Ser Val Glu Asn Ile Ala Arg Ile Phe Ser Pro Val Val Gly Ala
80               85               90

aaa att aac ccc aaa gat acg cca gaa acc tgg aat atg tta aag aat 458
Lys Ile Asn Pro Lys Asp Thr Pro Glu Thr Trp Asn Met Leu Lys Asn
95               100               105

ctt ctg aca atg ggc ggc tac tac gct act gct tcg gca aaa aaa tat 506
Leu Leu Thr Met Gly Gly Tyr Tyr Ala Thr Ala Ser Ala Lys Lys Tyr
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 Pro Glu Asp Glu Asn Thr Leu Arg Lys Asn Gly Ser Tyr Pro Ser Gly
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 cat act gct tat ggt aca ctt ctg gca tta gta tta tcc gag gcc aga 650
 His Thr Ala Tyr Gly Thr Leu Leu Ala Leu Val Leu Ser Glu Ala Arg
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 ccg gaa cgc gcg cag gag ctc gcc aga cgc gga tgg gag ttc ggg caa 698
 Pro Glu Arg Ala Gln Glu Leu Ala Arg Arg Gly Trp Glu Phe Gly Gln
 175 180 185
 agc aga gtg ata tgc ggt gct cac tgg caa agc gat gtt gat gct ggc 746
 Ser Arg Val Ile Cys Gly Ala His Trp Gln Ser Asp Val Asp Ala Gly
 190 195 200 205
 cgt tat gtg gga gca gta gag ttt gca aga ctg caa aca atc ccg gct 794
 Arg Tyr Val Gly Ala Val Glu Phe Ala Arg Leu Gln Thr Ile Pro Ala
 210 215 220
 ttt cag aag tca ctg gca aaa tcc gtg agg agc tgaacgacaa aaataattta 847
 Phe Gln Lys Ser Leu Ala Lys Ser Val Arg Ser
 225 230
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 gccacagcaa atgaaaggaa gtgcaactgc gtaggggcgg ccgggcgtgg agaatgcctt 967
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 35 40 45

Ala Tyr Arg Tyr Asp Lys Glu Ala Tyr Phe Lys Gly Tyr Ala Ile Lys
 50 55 60

Gly Ser Pro Arg Trp Lys Gln Ala Ala Glu Asp Ala Asp Val Ser Val
 65 70 75 80

Glu Asn Ile Ala Arg Ile Phe Ser Pro Val Val Gly Ala Lys Ile Asn
 85 90 95

Pro Lys Asp Thr Pro Glu Thr Trp Asn Met Leu Lys Asn Leu Leu Thr
 100 105 110

Met Gly Gly Tyr Tyr Ala Thr Ala Ser Ala Lys Lys Tyr Tyr Met Arg
 115 120 125

Thr Arg Pro Phe Val Leu Phe Asn His Ser Thr Cys Arg Pro Glu Asp
 130 135 140

Glu Asn Thr Leu Arg Lys Asn Gly Ser Tyr Pro Ser Gly His Thr Ala
 145 150 155 160

Tyr Gly Thr Leu Leu Ala Leu Val Leu Ser Glu Ala Arg Pro Glu Arg
 165 170 175

Ala Gln Glu Leu Ala Arg Arg Gly Trp Glu Phe Gly Gln Ser Arg Val
 180 185 190

Ile Cys Gly Ala His Trp Gln Ser Asp Val Asp Ala Gly Arg Tyr Val
 195 200 205

Gly Ala Val Glu Phe Ala Arg Leu Gln Thr Ile Pro Ala Phe Gln Lys
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Ser Leu Ala Lys Ser Val Arg Ser
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 ttttattaaa aggataggaa atgtcgtgaa atcggcattt tctatccata ttatataaca 300
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 Met Ile Lys Val Pro Arg Phe Ile Cys Met Ile Ala
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 Leu Thr Ser Gly Val Leu Ala Ser Gly Leu Ser Gln Ser Val Ser Ala
 15 20 25
 cat aca gaa aaa agt gaa ccc tcc tcg act tat cat ttc cac agc gat 448
 His Thr Glu Lys Ser Glu Pro Ser Ser Thr Tyr His Phe His Ser Asp
 30 35 40
 ccc ctt ctt tac ctt gcg ccc cca ccc act tcc ggc agt cca tta cag 496
 Pro Leu Leu Tyr Leu Ala Pro Pro Pro Thr Ser Gly Ser Pro Leu Gln
 45 50 55 60
 gcg cat gat gat caa acc ttt aac agc acc aga caa tta aaa ggt agc 544
 Ala His Asp Asp Gln Thr Phe Asn Ser Thr Arg Gln Leu Lys Gly Ser
 65 70 75
 acg cgc tgg gca ttg gca act caa gat gcc gat ctt cat ctc gct tca 592
 Thr Arg Trp Ala Leu Ala Thr Gln Asp Ala Asp Leu His Leu Ala Ser
 80 85 90
 gtt ctc aaa gac tat gcc tgc gcc gca gga atg aat ctc gat att gcg 640
 Val Leu Lys Asp Tyr Ala Cys Ala Ala Gly Met Asn Leu Asp Ile Ala
 95 100 105
 caa tta ccg cat ctt gcc aat ttg att aaa cgc gca ctt cgc acc gaa 688
 Gln Leu Pro His Leu Ala Asn Leu Ile Lys Arg Ala Leu Arg Thr Glu
 110 115 120

tat gac gat att ggc aga gcc aaa aat aac tgg aat cgc aaa cga cct 736
 Tyr Asp Asp Ile Gly Arg Ala Lys Asn Asn Trp Asn Arg Lys Arg Pro 140
 125 130 135

ttt gtg gat acc gat caa ccc atc tgc acg gaa aaa gat cgc gaa ggt 784
 Phe Val Asp Thr Asp Gln Pro Ile Cys Thr Glu Lys Asp Arg Glu Gly 155
 145 150

ctg gga aaa caa ggc tcc tat cct tca ggt cat acg act atc ggt tgg 832
 Leu Gly Lys Gln Gly Ser Tyr Pro Ser Gly His Thr Thr Ile Gly Trp 170
 160 165

agc gtt gcg ctc att ctg gct gaa ttg atc ccc gat cat gcg gcg aat 880
 Ser Val Ala Leu Ile Leu Ala Glu Leu Ile Pro Asp His Ala Ala Asn 185
 175 180

att ttg cag cgt ggc caa att ttt gga acc agc cgg att gtc tgc ggc 928
 Ile Leu Gln Arg Gly Gln Ile Phe Gly Thr Ser Arg Ile Val Cys Gly 200
 190 195

gcc cat tgg ttc agc gat gtg cag gca ggc tat atc atg gca tgc ggc 976
 Ala His Trp Phe Ser Asp Val Gln Ala Gly Tyr Ile Met Ala Ser Gly 220
 205 210 215

gaa att gca gct tta cat ggg gat gcc gat ttc cgc cga gat atg gaa 1024
 Glu Ile Ala Ala Leu His Gly Asp Ala Asp Phe Arg Arg Asp Met Glu 235
 225 230

tta gct cgg aaa gaa tta gaa aag gca cgc aca tca gcg cac acg cca 1072
 Leu Ala Arg Lys Glu Leu Glu Lys Ala Arg Thr Ser Ala His Thr Pro 250
 240 245

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 Asp Asp Leu Leu Cys Lys Ile Glu Gln Ser Ala Arg 260
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gaaaaaatga aagagcgcac gctctttcaa aggcaattcg atttagtccg gtggcattct 1238

caccgacaa accaaatcat aaataaccgc ctcttttccg ccagataact gaaaaattat 1298

agaataccga cagctggaat atcgctcactt ttcctag 1335

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 <213> *Zymomonas mobilis*

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20 25 30

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35 40 45

Leu Ala Pro Pro Pro Thr Ser Gly Ser Pro Leu Gln Ala His Asp Asp
50 55 60

Gln Thr Phe Asn Ser Thr Arg Gln Leu Lys Gly Ser Thr Arg Trp Ala
65 70 75 80

Leu Ala Thr Gln Asp Ala Asp Leu His Leu Ala Ser Val Leu Lys Asp
85 90 95

Tyr Ala Cys Ala Ala Gly Met Asn Leu Asp Ile Ala Gln Leu Pro His
100 105 110

Leu Ala Asn Leu Ile Lys Arg Ala Leu Arg Thr Glu Tyr Asp Asp Ile
115 120 125

Gly Arg Ala Lys Asn Asn Trp Asn Arg Lys Arg Pro Phe Val Asp Thr
130 135 140

Asp Gln Pro Ile Cys Thr Glu Lys Asp Arg Glu Gly Leu Gly Lys Gln
145 150 155 160

Gly Ser Tyr Pro Ser Gly His Thr Thr Ile Gly Trp Ser Val Ala Leu
165 170 175

Ile Leu Ala Glu Leu Ile Pro Asp His Ala Ala Asn Ile Leu Gln Arg
180 185 190

Gly Gln Ile Phe Gly Thr Ser Arg Ile Val Cys Gly Ala His Trp Phe

195

200

205

Ser Asp Val Gln Ala Gly Tyr Ile Met Ala Ser Gly Glu Ile Ala Ala
 210 215 220

Leu His Gly Asp Ala Asp Phe Arg Arg Asp Met Glu Leu Ala Arg Lys
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 245 250 255

Cys Lys Ile Glu Gln Ser Ala Arg
 260

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 catctectgt cattgcaatc ccgctatggt agcgcccaaa cggcaagggtg ataagtgcga 180
 cagtccgaaa tcgcgagtgg ttgctcatta agcagacaaa tatgcgtttt tgcgataccg 240
 aacaattttt tcaatgtgat tttaactttt acttacagat gacaaaaatg tgactaaaaa 300
 caaaaccatt gttctggaca tataacaccg taaggaaatg tag atg aaa aag cgc 355
 Met Lys Lys Arg
 -20

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Val Leu Ala Leu Cys Leu Ala Ser Leu Phe Ser Val Asn Ala Phe Ala
-15 -10 -5 -1

ctg gtc cct gcc ggc aat gat gca acc acc aaa ccg gat ctc tat tat 451
Leu Val Pro Ala Gly Asn Asp Ala Thr Thr Lys Pro Asp Leu Tyr Tyr
1 5 10 15

ctg aaa aat gca cag gcc atc gat agt ctg gcg ctg ttg ccg ccg ccg 499
Leu Lys Asn Ala Gln Ala Ile Asp Ser Leu Ala Leu Leu Pro Pro Pro
20 25 30

ccg gaa gtt ggc agc atc gca ttt tta aac gat cag gcg atg tat gag 547
Pro Glu Val Gly Ser Ile Ala Phe Leu Asn Asp Gln Ala Met Tyr Glu
35 40 45

aaa gga cgg ctg ttg cgc aat acc gaa cgt ggc aag cag gcg cag gca 595
Lys Gly Arg Leu Leu Arg Asn Thr Glu Arg Gly Lys Gln Ala Gln Ala
50 55 60

gat gct gac ctg gcc gcc ggc gac gtc gcg aat gcc ttc tcc agc gct 643
Asp Ala Asp Leu Ala Ala Gly Asp Val Ala Ala Phe Ser Ser Ala
65 70 75 80

ttt ggt tcg ccc atc acc gaa aaa gac gcg ccg cag tta cat aag ctg 691
Phe Gly Ser Pro Ile Thr Glu Lys Asp Ala Pro Gln Leu His Lys Leu
85 90 95

ctg aca aat atg att gag gat gcc ggc gat ctg gcc acc cgc agc gcg 739
Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala Thr Arg Ser Ala
100 105 110

aaa gag aaa tat atg cgc att cgc ccg ttt gcg ttc tac ggc gtt tca 787
Lys Glu Lys Tyr Met Arg Ile Arg Pro Phe Ala Phe Tyr Gly Val Ser
115 120 125

acc tgt aac act aaa gac cag gac aag ctg tcg aaa aac gga tct tac 835
Thr Cys Asn Thr Lys Asp Gln Asp Lys Leu Ser Lys Asn Gly Ser Tyr
130 135 140

cct tcc ggc cat acc tct acc ggt tgg gca acc gcg ctg gta ctg gcg 883
Pro Ser Gly His Thr Ser Thr Gly Trp Ala Thr Ala Leu Val Leu Ala
145 150 155 160

gag atc aat ccg cag cgg caa aac gaa att ctc aaa cgc ggc tat gaa 931
Glu Ile Asn Pro Gln Arg Gln Asn Glu Ile Leu Lys Arg Gly Tyr Glu
165 170 175

ttg ggc gaa agc cgg gtt atc tgc ggc tat cat tgg cag agc gat gtc 979
Leu Gly Glu Ser Arg Val Ile Cys Gly Tyr His Trp Gln Ser Asp Val

180	185	190	
gat gcg gcg cgg ata gtc ggc tgc gcg gtg gtg gcg acc ctg cat acc			1027
Asp Ala Ala Arg Ile Val Gly Ser Ala Val Val Ala Thr Leu His Thr			
195	200	205	
aac ccg gcc ttc caa cag cag ttg cag aaa gca aag gat gaa ttc gcc			1075
Asn Pro Ala Phe Gln Gln Gln Leu Gln Lys Ala Lys Asp Glu Phe Ala			
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Lys Thr Gln Lys			
225			
gcgcctttctc cgggctacta aatcgcacag cgctgtagcc ccggtaaagc ccagcgccac			1187
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Asp Leu Tyr Tyr Leu Lys Asn Ala Gln Ala Ile Asp Ser Leu Ala Leu			
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 30 35 40

Ala Met Tyr Glu Lys Gly Arg Leu Leu Arg Asn Thr Glu Arg Gly Lys
 45 50 55 60

Gln Ala Gln Ala Asp Ala Asp Leu Ala Ala Gly Asp Val Ala Asn Ala
 65 70 75

Phe Ser Ser Ala Phe Gly Ser Pro Ile Thr Glu Lys Asp Ala Pro Gln
 80 85 90

Leu His Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala
 95 100 105

Thr Arg Ser Ala Lys Glu Lys Tyr Met Arg Ile Arg Pro Phe Ala Phe
 110 115 120

Tyr Gly Val Ser Thr Cys Asn Thr Lys Asp Gln Asp Lys Leu Ser Lys
 125 130 135 140

Asn Gly Ser Tyr Pro Ser Gly His Thr Ser Thr Gly Trp Ala Thr Ala
 145 150 155

Leu Val Leu Ala Glu Ile Asn Pro Gln Arg Gln Asn Glu Ile Leu Lys
 160 165 170

Arg Gly Tyr Glu Leu Gly Glu Ser Arg Val Ile Cys Gly Tyr His Trp
 175 180 185

Gln Ser Asp Val Asp Ala Ala Arg Ile Val Gly Ser Ala Val Val Ala
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Thr Leu His Thr Asn Pro Ala Phe Gln Gln Gln Leu Gln Lys Ala Lys
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 <220>
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 <210> 116
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 <210> 119
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 <210> 120
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 <210> 121
 <211> 9
 <212> PRT
 <213> Artificial Sequence

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 <223> acid phosphatase motif

 <220>
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 <222> (2)..(7)
 <223> Xaa = any amino acid

 <400> 121

 Lys Xaa Xaa Xaa Xaa Xaa Xaa Arg Pro
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<210> 122
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 <213> Artificial Sequence

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 <223> acid phosphatase motif
 <400> 122

Pro Ser Gly His
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Ser Arg Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Asp
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<210> 124
 <211> 231
 <212> PRT
 <213> Escherichia blattae

<400> 124

Leu Ala Leu Val Ala Thr Gly Asn Asp Thr Thr Thr Lys Pro Asp Leu
 1 5 10 15

Tyr Tyr Leu Lys Asn Ser Glu Ala Ile Asn Ser Leu Ala Leu Leu Pro

20

25

30

Pro Pro Pro Ala Val Gly Ser Ile Ala Phe Leu Asn Asp Gln Ala Met
35 40 45

Tyr Glu Gln Gly Arg Leu Leu Arg Asn Thr Glu Arg Gly Lys Leu Ala
50 55 60

Ala Glu Asp Ala Asn Leu Ser Ser Gly Gly Val Ala Asn Ala Phe Ser
65 70 75 80

Gly Ala Phe Gly Ser Pro Ile Thr Glu Lys Asp Ala Pro Ala Leu His
85 90 95

Lys Leu Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala Thr Arg
100 105 110

Ser Ala Lys Asp His Tyr Met Arg Ile Arg Pro Phe Ala Phe Tyr Gly
115 120 125

Val Ser Thr Cys Asn Thr Thr Glu Gln Asp Lys Leu Ser Lys Asn Gly
130 135 140

Ser Tyr Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala Leu Val
145 150 155 160

Leu Ala Glu Ile Asn Pro Gln Arg Gln Asn Glu Ile Leu Lys Arg Gly
165 170 175

Tyr Glu Leu Gly Gln Ser Arg Val Ile Cys Gly Tyr His Trp Gln Ser
180 185 190

Asp Val Asp Ala Ala Arg Val Val Gly Ser Ala Val Val Ala Thr Leu
195 200 205

His Thr Asn Pro Ala Phe Gln Gln Gln Leu Gln Lys Ala Lys Ala Glu
210 215 220

Phe Ala Gln His Gln Lys Lys
 225 230

<210> 125
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 <212> PRT
 <213> Enterobacter aerogenes

<400> 125

Leu Val Pro Ala Gly Asn Asp Ala Thr Thr Lys Pro Asp Leu Tyr Tyr
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Leu Lys Asn Ala Gln Ala Ile Asp Ser Leu Ala Leu Leu Pro Pro Pro
 20 25 30

Pro Glu Val Gly Ser Ile Ala Phe Leu Asn Asp Gln Ala Met Tyr Glu
 35 40 45

Lys Gly Arg Leu Leu Arg Asn Thr Glu Arg Gly Lys Leu Ala Ala Glu
 50 55 60

Asp Ala Asn Leu Ser Ala Gly Gly Val Ala Asn Ala Phe Ser Ser Ala
 65 70 75 80

Phe Gly Ser Pro Ile Thr Glu Lys Asp Ala Pro Gln Leu His Lys Leu
 85 90 95

Leu Thr Asn Met Ile Glu Asp Ala Gly Asp Leu Ala Thr Arg Ser Ala
 100 105 110

Lys Glu Lys Tyr Met Arg Ile Arg Pro Phe Ala Phe Tyr Gly Val Ser
 115 120 125

Thr Cys Asn Thr Thr Glu Gln Asp Lys Leu Ser Lys Asn Gly Ser Tyr
 130 135 140

Pro Ser Gly His Thr Ser Ile Gly Trp Ala Thr Ala Leu Val Leu Ala
 145 150 155 160

Glu Ile Asn Pro Gln Arg Gln Asn Glu Ile Leu Lys Arg Gly Tyr Glu
 165 170 175

Leu Gly Glu Ser Arg Val Ile Cys Gly Tyr His Trp Gln Ser Asp Val
 180 185 190

Asp Ala Ala Arg Ile Val Gly Ser Ala Val Val Ala Thr Leu His Thr
 195 200 205

Asn Pro Ala Phe Gln Gln Gln Leu Gln Lys Ala Lys Asp Glu Phe Ala
 210 215 220

Lys Thr Gln Lys
 225